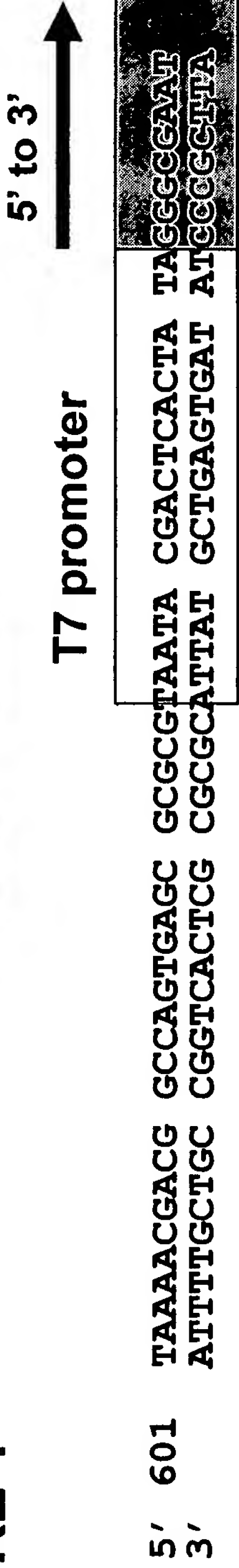


FIGURE 1

EXHIBIT A



5' GGGCGAAU

1. Hae III cleavage of plasmid *plus* T3 polymerase transcription
2. Pvu II cleavage of plasmid *plus* T7 polymerase transcription

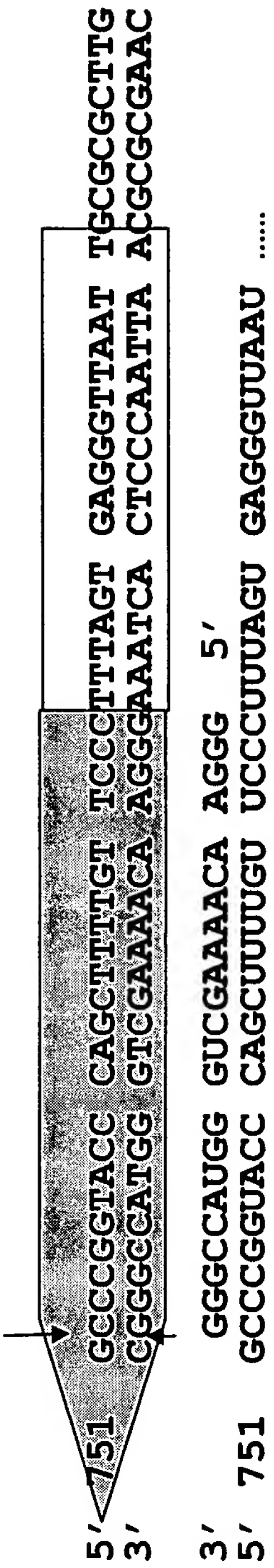
5' 651 TGGAGCTCCA CCGCGGTGGC GGCCGCTCTA GAACTAGTGG ATCCCCCGGG  
3' ACCTCGAGGT GCGGCCACCG CCGCGGAGAT CTGATCATT TAGGGGGCCC

5' UGGUGCUCCA CCGCGGUGGC GGCCGCUCUA GAACUAGUGG AUCCCCCGGG

5' 701 CTGCAGGAAT TCGATATCAA GCTTATCGAT ACCGTCGACC TCGAGGGGGG  
3' GACGTTCTTA AGCTATAGTT CGAATAGCTA TGGCAGCTGG AGTCCCCCCC

5' CUGCAGGAU UCGAUACA GCUUAUCGAU ACCGUCGACC UCGAGGGGGG

Hae III



# EXHIBIT A

FIGURE 2A

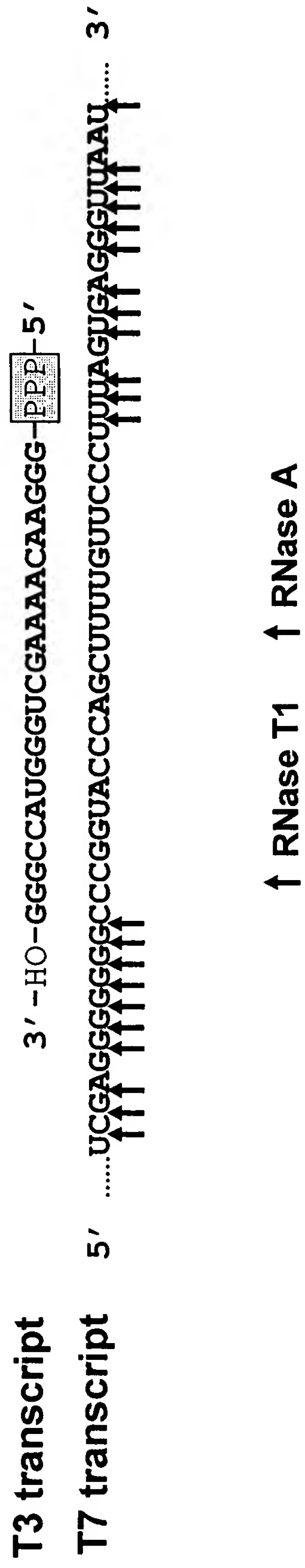


FIGURE 2B



EXHIBIT A

Transcript 3' end  
Heterogeneity  
(Size Range (nt))

Yes  
(100-104+)

Yes  
(81-85+)

Yes  
(63-67+)

Yes  
(51-55+)

Yes  
(36-40+)

Yes  
(30-34+)

Template 5' End  
(top strand = template strand)

3' ←----- 5'  
104 100  
5' -GGCCGCTCTAG-3'  
CGAGATC-5'

3' ←----- 5'  
85 81  
5' -GATCCCCCGG-3'  
CGGGCCC-5'

3' ←----- 5'  
67 63  
5' -AATTCGAATC-3'  
TTAAGCT-5'

3' ←----- 5'  
55 51  
5' -AGCTTATCGAT-3'  
ATAGCTA-5'

3' ←----- 5'  
40 36  
5' -TCGACCTCGAG-3'  
GGAGCTC-5'

3' ←----- 5'  
34 30  
5' -TCGAGGGGGG-3'  
CCCCCCC-5'

Restriction Digest  
(+HaeIII)

Eag I  
↓ CGGCCG  
GCCGGC

BamH1  
↓ GGATCC  
CCTAGG

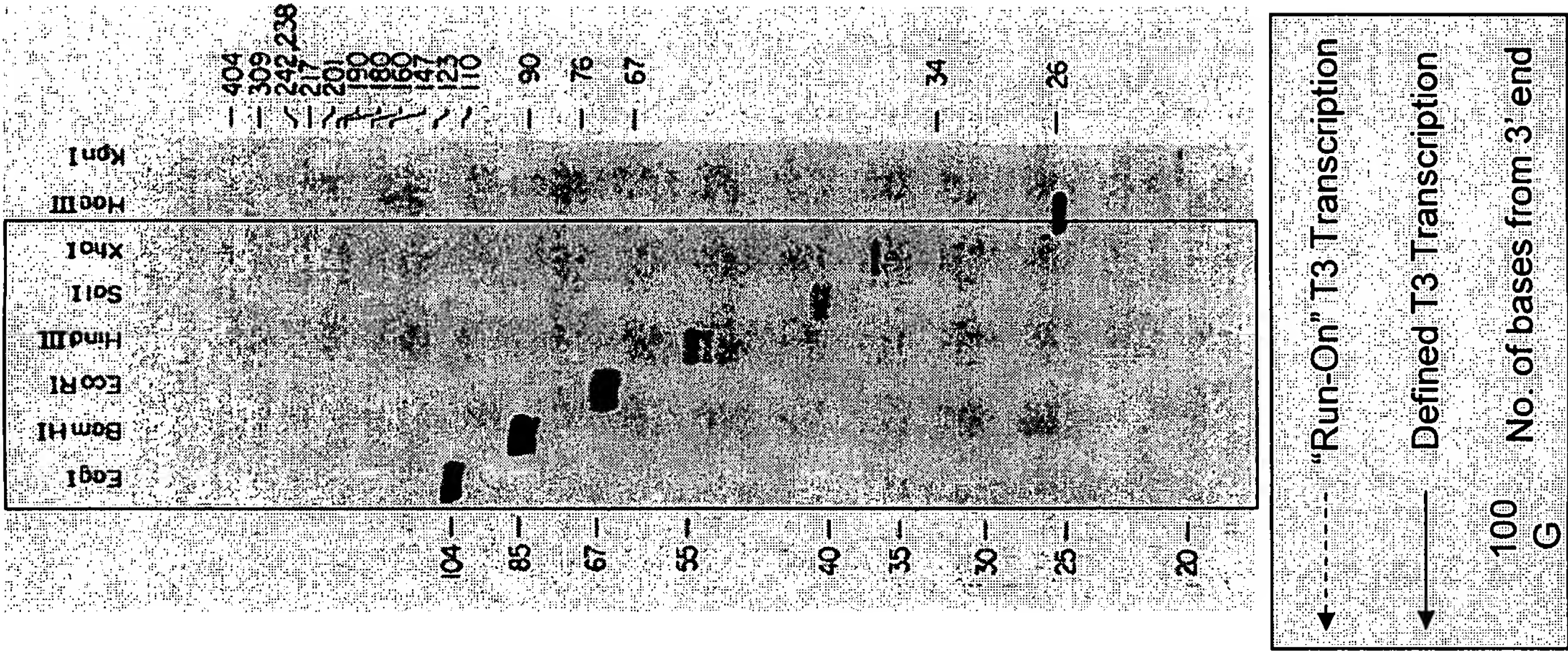
EcoR1  
↓ GAATTC  
CCTAGG

HindIII  
↓ AAGCTT  
TTCGAA

Sal I  
↓ GTCGAC  
CAGCTG

Xho I  
↓ CTCGAG  
GAGCTC

FIGURE 3A





# FIGURE 3B

# EXHIBIT A

